



PC

RE-RUN

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/529,624

DATE: 02/06/2006

TIME: 11:05:26

Input Set : A:\0267us310 sequence.2-revJRP.txt

Output Set: N:\CRF4\02012006\J529624.raw

3 <110> APPLICANT: Haaning, Jesper Mortensen et al.; Maxygen Holdings Ltd.
5 <120> TITLE OF INVENTION: FVII or FVIIa variants having increased clotting activity
7 <130> FILE REFERENCE: 0267us310
-> 9 <140> CURRENT APPLICATION NUMBER: US/10/529,624
-> 10 <141> CURRENT FILING DATE: 2005-03-30
12 <150> PRIOR APPLICATION NUMBER: US 60/479,642
13 <151> PRIOR FILING DATE: 2003-06-19
15 <150> PRIOR APPLICATION NUMBER: US 60/414,836
16 <151> PRIOR FILING DATE: 2002-09-30
18 <160> NUMBER OF SEQ ID NOS: 34
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 406
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
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29 1 5 10 15
30 Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys
31 20 25 30
32 Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
33 35 40 45
34 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
35 50 55 60
36 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
37 65 70 75 80
38 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
39 85 90 95
40 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
41 100 105 110
42 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
43 115 120 125
44 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
45 130 135 140
46 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
47 145 150 155 160
48 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
49 165 170 175
50 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
51 180 185 190
52 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
53 195 200 205
54 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg

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55      210      215      220
56 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
57 225      230      235      240
58 His Asp Ile Ala Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
59      245      250      255
60 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
61      260      265      270
62 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
63      275      280      285
64 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
65      290      295      300
66 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
67 305      310      315      320
68 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
69      325      330      335
70 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
71      340      345      350
72 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
73      355      360      365
74 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
75      370      375      380
76 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
77 385      390      395      400
78 Leu Arg Ala Pro Phe Pro
79      405
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 1338
84 <212> TYPE: DNA
85 <213> ORGANISM: Homo sapiens
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (115)..(1335)
91 <400> SEQUENCE: 2
92 atgggtcagcc aggcctctcgc cctcctgtgc ctgctcctgg ggctgcaggg ctgcctggct 60
94 gccgtcttcg tcaccagga ggaagccat ggcgtcctgc atcgccggcg ccgg gcc 117
95      Ala
96      1
98 aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165
99 Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
100      5      10      15
102 aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213
103 Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
104      20      25      30
106 gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261
107 Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
108      35      40      45
110 tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg 309
111 Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu
112 50      55      60      65
```

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114	cag	agc	tat	atc	tgc	ttc	tgc	ctg	cct	gcc	ttt	gag	ggg	cgc	aat	tgc	357
115	Gln	Ser	Tyr	Ile	Cys	Phe	Cys	Leu	Pro	Ala	Phe	Glu	Gly	Arg	Asn	Cys	
116					70					75					80		
118	gaa	acc	cat	aag	gat	gac	cag	ctg	att	tgc	gtc	aac	gaa	aac	ggg	ggc	405
119	Glu	Thr	His	Lys	Asp	Asp	Gln	Leu	Ile	Cys	Val	Asn	Glu	Asn	Gly	Gly	
120				85					90					95			
122	tgc	gag	cag	tac	tgc	agc	gat	cac	acg	ggc	acg	aag	cgg	agc	tgc	cgc	453
123	Cys	Glu	Gln	Tyr	Cys	Ser	Asp	His	Thr	Gly	Thr	Lys	Arg	Ser	Cys	Arg	
124				100					105				110				
127	tgc	cac	gaa	ggc	tat	agc	ctc	ctg	gct	gac	ggg	gtg	tcc	tgc	acg	ccc	501
128	Cys	His	Glu	Gly	Tyr	Ser	Leu	Leu	Ala	Asp	Gly	Val	Ser	Cys	Thr	Pro	
129		115					120					125					
131	acg	gtg	gaa	tac	cct	tgc	ggg	aag	att	ccc	att	cta	gaa	aag	cgg	aac	549
132	Thr	Val	Glu	Tyr	Pro	Cys	Gly	Lys	Ile	Pro	Ile	Leu	Glu	Lys	Arg	Asn	
133	130					135					140					145	
135	gct	agc	aaa	ccc	cag	ggc	cgg	atc	gtc	ggc	ggg	aag	gtc	tgc	cct	aag	597
136	Ala	Ser	Lys	Pro	Gln	Gly	Arg	Ile	Val	Gly	Gly	Lys	Val	Cys	Pro	Lys	
137				150						155					160		
139	ggg	gag	tgc	ccc	tgg	cag	gtc	ctg	ctc	gtc	aac	ggg	gcc	cag	ctg		645
140	Gly	Glu	Cys	Pro	Trp	Gln	Val	Leu	Leu	Leu	Val	Asn	Gly	Ala	Gln	Leu	
141				165					170					175			
143	tgc	ggc	ggg	acc	ctc	atc	aat	acc	att	tgg	gtc	gtg	tcc	gcc	gct	cac	693
144	Cys	Gly	Gly	Thr	Leu	Ile	Asn	Thr	Ile	Trp	Val	Val	Ser	Ala	Ala	His	
145			180					185					190				
147	tgc	ttc	gat	aag	att	aag	aat	tgg	cgg	aac	ctc	atc	gct	gtg	ctc	ggc	741
148	Cys	Phe	Asp	Lys	Ile	Lys	Asn	Trp	Arg	Asn	Leu	Ile	Ala	Val	Leu	Gly	
149		195					200				205						
151	gaa	cac	gat	ctg	tcc	gag	cat	gac	ggg	gac	gaa	cag	tcc	cgc	cgg	gtg	789
152	Glu	His	Asp	Leu	Ser	Glu	His	Asp	Gly	Asp	Glu	Gln	Ser	Arg	Arg	Val	
153	210					215				220					225		
155	gct	cag	gtc	atc	att	ccc	tcc	acc	tat	gtg	cct	ggc	acg	acc	aat	cac	837
156	Ala	Gln	Val	Ile	Ile	Pro	Ser	Thr	Tyr	Val	Pro	Gly	Thr	Thr	Asn	His	
157				230						235					240		
159	gat	atc	gct	ctg	ctc	cgc	ctc	cac	cag	ccc	gtc	gtg	ctc	acc	gat	cac	885
160	Asp	Ile	Ala	Leu	Leu	Arg	Leu	His	Gln	Pro	Val	Val	Leu	Thr	Asp	His	
161				245					250					255			
163	gtc	gtg	cct	ctg	tgc	ctg	cct	gag	cgg	acc	ttt	agc	gaa	cgc	acg	ctg	933
164	Val	Val	Pro	Leu	Cys	Leu	Pro	Glu	Arg	Thr	Phe	Ser	Glu	Arg	Thr	Leu	
165				260				265					270				
167	gct	ttc	gtc	cgc	ttt	agc	ctc	gtg	tcc	ggc	tgg	ggc	cag	ctg	ctc	gac	981
168	Ala	Phe	Val	Arg	Phe	Ser	Leu	Val	Ser	Gly	Trp	Gly	Gln	Leu	Leu	Asp	
169		275					280				285						
171	cgg	ggc	gct	acc	gct	ctc	gag	ctg	atg	gtg	ctc	aac	gtc	ccc	cgg	ctg	1029
172	Arg	Gly	Ala	Thr	Ala	Leu	Glu	Leu	Met	Val	Leu	Asn	Val	Pro	Arg	Leu	
173	290					295				300					305		
175	atg	acc	cag	gac	tgc	ctg	cag	cag	tcc	cgc	aaa	gtg	ggg	gac	tcc	ccc	1077
176	Met	Thr	Gln	Asp	Cys	Leu	Gln	Gln	Ser	Arg	Lys	Val	Gly	Asp	Ser	Pro	
177				310					315					320			
179	aat	atc	acg	gag	tat	atg	ttt	tgc	gct	ggc	tat	agc	gat	ggc	tcc	aag	1125

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180 Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys
181          325          330          335
183 gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc 1173
184 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
185          340          345          350
187 ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc 1221
188 Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala
189          355          360          365
191 acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag 1269
192 Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu
193 370          375          380          385
195 tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg 1317
196 Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu
197          390          395          400
199 cgg gcc cct ttc cct tga taa 1338
200 Arg Ala Pro Phe Pro
201          405
204 <210> SEQ ID NO: 3
205 <211> LENGTH: 31
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
212 <400> SEQUENCE: 3
213 agctggctag ccactgggca ggtaagtatc a 31
216 <210> SEQ ID NO: 4
217 <211> LENGTH: 31
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
224 <400> SEQUENCE: 4
225 tggcgggata ctttaagagct gtaattgaac t 31
228 <210> SEQ ID NO: 5
229 <211> LENGTH: 23
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
236 <400> SEQUENCE: 5
237 tcagctcgag agcggtagcg ccc 23
240 <210> SEQ ID NO: 6
241 <211> LENGTH: 38
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
248 <400> SEQUENCE: 6
249 cccattctag aaaagcggaa cgccagcaaa ccccaggg 38
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Input Set : A:\0267us310 sequence.2-revJRP.txt

Output Set: N:\CRF4\02012006\J529624.raw

252 <210> SEQ ID NO: 7
253 <211> LENGTH: 30
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
260 <400> SEQUENCE: 7
261 gctgagcgga ccaaacactt ttggattagc 30
264 <210> SEQ ID NO: 8
265 <211> LENGTH: 30
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
272 <400> SEQUENCE: 8
273 gctaataccaa aagtgttttg tccgctcagc 30
276 <210> SEQ ID NO: 9
277 <211> LENGTH: 30
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
284 <400> SEQUENCE: 9
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288 <210> SEQ ID NO: 10
289 <211> LENGTH: 30
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
296 <400> SEQUENCE: 10
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302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
308 <400> SEQUENCE: 11
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313 <211> LENGTH: 30
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
320 <400> SEQUENCE: 12
321 cgccatcgct atactgaatc caaaacagtt 30
324 <210> SEQ ID NO: 13

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/529,624

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9 M:270 C: Current Application Number differs, Replaced Current Application Number
10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

STATISTICS SUMMARY

PATENT APPLICATION: US/10/529,624

DATE: 02/06/2006

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Input Set : A:\0267us310 sequence.2-revJRP.txt

Output Set : N:\CRF4\02012006\J529624.raw

Application Serial Number: US/10/529,624

Application Class: Numeric or Numeric or Xml: Numeric

Application Class:

Application File Date: 03-30-2005

Unit: PCT

Software Application: PatentIN2.1

Total Number of Sequences: 34

Total Nucleotides: 2317

Total Amino Acids: 406

Number of Errors: 0

Number of Warnings: 0

Number of Corrections: 2

MESSAGE SUMMARY

1 C: 1 (Current Application Number differs)

1 C: 1 (Current Filing Date differs)